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QST9Y4 HUMAN
ID QST9Y4;
AC QST9Y4;
AC QST9Y4;
DT 01-FEB-2005 (TrEMBLrel. 29,
DE Undor necrosis factors (Eleman).
OC NAMMERT (Human).
OC BUKARYOLS; Metazon; Chordat,
OC Mammalia; Eutheria; Euarcholoc,
OC MAMMERT (Human).
OC HOMO.
OC HOMO.
OC HOMO.
OC NCBI_TAXID-9606;
RN [1]
RP WUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the
DR GO; GO:0016020; C:membrane;
DR GO; GO:0016020; F:tumor nec
DR GO; GO:0016020; S:tumor nec
FT NON TER 317
SQ SEQUENCE 317 AA; 35478 M
                       RESULT 3
TO TWELL MOUSE STANDARD; PRT; 316 AA.

AC 035235; 035306; Q9JJK8; Q9JJK9; Q9RIY0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Lest sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator temporal factor ligand) (RAMK) (TMF-related activation-defined cytokine) (TRANCE) (Osteoprotegerin ligand) (OPG) (OSTEOPROTEGEN) (OSTEOPROTEGEN) (OPG) (OSTEOPROTEGEN) (OPG) (OSTEOPROTEGEN) (OPG) (OSTEOPROTEGEN) (OSTEOPROTE
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Tumor necrosis factor (Ligand) superfamily, member 11
Name=TNFSF11; ORFNames=RP11-86N24.2-001;
Homo saptens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EuMammalia; Eutheria; Euarchontoglires; Primates; Catarr
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MEDLINE=21464816; Publicam J., Nelson C.A., I "Crystal structure of
                                                               PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION. WEDLINB-99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613; Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H. Schloendorff J., Tempst P., Choi Y., Blobel C.P.; "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha) converting enzyme-like protease in shedding of TRANCE, a TNF fami member involved in osteoclastogenesis and dendritic cell surviva." Biol. Chem. 274:13613-13618(1999).
                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor
factor-kappaB ligand and their differential expre
                                                                                                                                                                                                                                                                                                                         "Cloning and characterization differentiation factor."; Gene 230:121-127(1999).
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MEDLINE-98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;

Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,

Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., 7

Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;

"Osteoclast differentiation factor is a ligand for

osteoprotegerin/osteoclastogenesis-inhibitory factor and is ic

to TRANCE/RANKL.";

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Ueda M., Higashio K.;
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Kodaira K., Kodaira K., Mizuno A.,
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WEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;

Anderson D.M., Maraskovsky E., Billingsley W.L., Doug
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Coalibert L.;
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"TRANCE is a novel ligand of the tumor that activates c-Jun N-terminal kinase J. Biol. Chem. 272:25190-25194(1997).
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TISSUE-Hybridoma;

MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;

Mond B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,

Lee
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                               PubMed=11581298
ROSS F.P., Teitelk
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DOI=10.1210/en.142.4.1419;
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Yasuda H., Shima N., Murakami A.,
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Teitelbaum S.L., 3/RANKL cytokine

reveals c

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receptor-ligand specificity."; Clin. Invest. 108:971-979(2001).

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REMBL; AP013170; AAC71061.1; -; mRNA.

REMBL; AP013048; AAB86812.1; -; mRNA.

REMBL; AP053713; AAC30113.1; -; mRNA.

REMBL; AB002845; BAA25425.1; -; mRNA.

REMBL; AB0022039; BAA36970.1; -; Genomic DNA.

REMBL; AB0022771; BAA397257.1; -; mRNA.

REMBL; AB032772; BAA397257.1; -; mRNA.

REMBL; AB032772; BAA397259.1; -; mRNA.

REMBL; AB032771; BAA397259.1; -; mRNA.

REMBL; AB03271; C:integral to membrane; TAS.

REMBL; AB032771; BAA37259.1; -; mRNA.

REMBL; AB03271; P:DOSETETON; IMP.

REMBL; AB03271; BAA37259.1; -; mRNA.

REMBL; AB03271; BAA37259.1; -; mRNA.

REMBL; AB03271; BAA37259.1; -; mRNA.

REMBL; AB03271; P:DOSETETON; IMP.

REMBL; AB03271; BAA37259.1; -; mRNA.

REMBL; AB03271; BAA37259.1; -; mRNA.

REMBL; AB032071; P:DOSETETON; IMP.

REMBL; AB032071; P:DOSETETON; IDA.

REMBL; AB03201; P:DOSETON; IDA.

REMBL; A
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J. Biol. Chem. 277:6631-6636(2002).

C. INPREPILA/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell poroliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

C. --- SUBCLIUTAR LOCATION: Type II membrane protein and secreted (1soforms 1 and 2). Cytoplasmic (1soforms 3).

C. --- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
use as long as its content is in no way modified and this stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by proteolytic processing. The cleavage may be catalyzed by ADAMI? A further shorter soluble form was observed. DISEASE: Deficiency in Thfsfil results in failure to form lobulo-alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick, irregular growth plates and a relative increase in hypertrophic chondrocytes.

SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=035235-3; Sequence=VSP 006448;
TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes, but not in nonlymphoid tissues and is abundantly expressed in T cells but not in B cells. A high level expression is also seen the trabecular bone and lung.

PTM: N-glycosylated.

PTM: The soluble form of isoform 1 derives from the membrane form.
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SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003636; TNF_subf
Pfam; PF00229; TNF; 1.
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268; Conser
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Pred. No. 5.7e-113;
6; Mismatches 31;
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G -> D (in Ref. 2).
Missing (in Ref. 5)
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Extracellular (Potential).
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member 11, membrane form.
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"Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNFSF11 (TRANCE, RANKI, ODF, OPGL) gene.";

Int. J. Dev. Biol. 45:853-859(2001).

-I- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in nenhanced bone-resorption in humoral
                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                     similarity).

-i- TISSUB SPECIFICITY: Highly expressed in thymus and bone tissues.

-i- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-i- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Safadi F.F., Popoff S.N., Lengner C., van-Hul W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21662371; PubMed=11804028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20540945; PubMed=11092398; Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Tibial bone;
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bone
                                                                                                                                                                                                                                                                                                                      hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
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27; Conservative
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Pred. No. 2.1e-12;
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                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 314:1021-1027(2004)
EMBL; AB064268; BAB79693.1; -; mRNA.
Receptor.
                                                                                                                                                                                                                                                                                                                                                           PubMed=14751235; DOI=10.1016/j.bbrc.2003.12.191; Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Ut Tatsumi M., Uematsu H., Hirokawa K.; "Regulation of osteoclastogenesis by three human RANKL expressed in NIH3F3 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Receptor activator of nuclear factor kappa B ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q54A98 HUMAN PRELIMINARY;
Q54A98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CONFLICT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=hRANKL 3;
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PROSITE; PS50049; TNF 2; 1.

Cytokine; Developmental protein; Differentiation; Glycoprotein; Receptor; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGD; 620784; Tnf8f11.
GO; GO:0045780; P:positive regulation of bone resorption; IMP.
GO; GO:0045672; P:positive regulation of osteoclast different.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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HSSP; 035235; 1JTZ.
SMR; Q9ESE2; 163-318.
Ensembl; ENSRNOG00000009559; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00229; TNF;
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InterPro; IPR003636; TNF_subf.
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                                   μ
                                                                                                                                      Similarity
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25; Conserv
NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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                                                                                                                                                                                                                                         244 AA;
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                                                                                                   Conservative
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141 Cleavage (By similarity).
199 N-linked (GlCNAC. . . ) (Pc
264 N-linked (GlCNAC. . . ) (Pc
317 I -> M (in Ref 2).
35370 MW; 4B87A4D706AD098F CRC64;
                                                                                                                                                                                                                                         27690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Buteleostomi; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318
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68
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                                                                                            ; Score 136; DB
; Pred. No. 7.8e
1; Mismatches
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Extracellular (Potential).
Cleavage (By similarity).
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
I -> M (in Ref. 2).
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Pred. No. 2.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          member 11, membrane form.
Tumor necrosis factor ligand superfamily member 11, soluble form.
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                                                                                                                                                                                                                                  C827590684B6B83C CRC64;
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7.8e-1
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DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activator DE induced cytokine) (TRANCB) (Ostcoprotegerin ligand) (OPGL) (Ostcoclast DE differentiation factor) (ODP) (Contains: Tumor necrosis factor ligand B superfamily member 11, membrane form; Tumor necrosis factor ligand DE superfamily member 11, soluble form; Tumor necrosis factor ligand DR superfamily member 11, soluble form; Ratus norvegicus (Rat).

C Mamman, Metazoa. C.
TRESULT RESULT REPORT OF THE TRESULT REPORT 
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21662371; PubMed-11804028;
Odgren P.R., Kim N., van Wesenbeeck L., MacKay C.,
Safadi F.F., Popoff S.N., Lengner C., van-Hul W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 266-318
STRAIN-Fischer 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, sequence and functional characterization homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20540945; PubMed=11092398; Xu J.K., Tan J.K., Huang L., Gao X.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Tibial bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marks S.C. Jr.;
"Evidence that the rat osteopetrotic mutation toothless (tl)
"Evidence that the rat osteopetrotic mutation toothless (tl)
the TMPSP11 (TRANCE, RANKL, ODF, OPGL) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
     EMBL, AF187319,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the TNFSF11 (TRANCE, RANKL, ODF, OF INT. J. Dev. Biol. 45:853-859(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zheng M.H.;
                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Cytckine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

SUBCELLULAR LOCATION: Type II membrane protein and secreted (By SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                          proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                  Buropean Bioinformatics Institute.
as long as its content is in no way
                                                                                                                                                                                                                                                                                                             TISSUE
                                                                                                                                                                                                                                                                                      PTM: The soluble form derives from the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
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                                                                                                                                                                                                                                                                                                             SPECIFICITY: Highly expressed in thymus
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     AAG17031.1; -;
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Pred. No. 3.4e-06;
     mRNA
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                                                                                        modified and
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Choi Y∵,
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPO_DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPO DOM
                                                                                                                     Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q54A98;
13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00251; TNF 1; FALSE NEG PROSITE; PS50049; TNF 2; 1.
Cytokine; Developmental protein; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002012; TNI
SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMR; O9ESE2; 163-318.
Ensembl; ENSRNOG00000009559; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF425669; AAL23963.1; -; mRNA
HSSP; O35235; lJTZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q54A98_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Signal-anchor; CHAIN 1 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGD; 620784; Tnfsf11.
GO; GO:0045780; P:positive regulation
GO; GO:0045672; P:positive regulation
InterPro; IPR006052; TNF_family.
InterPro; IPR03336; TNF_subf.
                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
PubMed=14751235; DOI=10.1016/j.bbrc.2003.12.191;
Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai
Tatsumi M., Uematsu H., Hirokawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                   "Regulation of osteoclastogenesis expressed in NIH3T3 cells.";
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=hRANKL 3;
                                                                                                                                                              EMBL; AB064268; BAB79693.1; -;
                                                                                                                                                                                Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                          Omo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens (Human)
                                                                                                                                                                                                                                                                                                                                            TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conser
                                             15;
                                                             Similarity
                                                                                                                                                                                Biophys. Res. Commun. 314:1021-1027(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYVVKTSIKIPSSHNLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYVVKTSIKIPSSHNLM 17
        VYVVKTSIKIPSSHNLM 17
                                                                                                                         244 AA;
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(TIRMBLrel. 31, Last sequence update)
(TIRMBLrel. 31, Last annotation updat
ivator of nuclear factor kappa B liga
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                                               Conservative
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68
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Euarchontoglires; Primates;
                                                                                                                         27690 MW;
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                                             0
                                                               Score
Pred.
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N-linked (GlcNAc. ..) (Potential)
I -> M (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
Signal-anchor for type II |
protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  member 11, membrane form.
Tumor necrosis factor ligand
member 11, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage (By similarity)
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                                                                                                                           C827590684B6B83C CRC64;
                                               Mismatches
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                                                                                                                                                                                                                         ş
                                                               74;
No.
                                                                                                                                                                                                                         three human
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                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi; rimates; Catarrhini; Hominidae;
                                                                                      BB
                                                                 .00015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligand
                                                                                  Length 244
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                                               Indels
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